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<p>(71) Applicant: DIVERSA CORPORATION [US/US]; 10665 Sorrento Valley Road, San Diego, CA 92121 (US).</p> <p>(72) Inventor: KRETZ, Keith; 973 Hawthorne Drive, San Marcos, CA 92069 (US).</p> <p>(74) Agent: HAILE, Lisa, A.; Fish &amp; Richardson P.C., Suite 1400, 4225 Executive Square, La Jolla, CA 92037 (US).</p>			
<p>(54) Title: NOVEL PHYTASE</p>			
<p>(57) Abstract</p> <p>The invention provides a purified phytate enzyme derived from <i>Escherichia coli</i> B. The enzyme has a molecular weight of about 47.1 kilodaltons and has phytase activity (SEQ ID NO:2). The enzyme can be produced from native or recombinant host cells and can be used to aid in the digestion of phytate where desired. In particular, the phytase of the present invention can be used in animal feed.</p>			

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## NOVEL PHYTASE

Field of the Invention

This invention relates to newly identified polynucleotides, polypeptides encoded by such polynucleotides, the use of such polynucleotides and polypeptides, as well as the production and isolation of such polynucleotides and polypeptides. More particularly, the polypeptides of the present invention have been identified as phytases and in particular, enzymes having phytase activity.

Background

Minerals are essential elements for the growth of all organisms. For livestock production of monogastric animals (e.g., pigs, poultry) and fish, feed is commonly supplemented with minerals. Plant seeds are a rich source of minerals since they contain ions that are complexed with the phosphate groups of phytic acid. Ruminants do not require inorganic phosphate and minerals because microorganisms in the rumen produce enzymes that catalyze conversion of phytate (myo-inositol-hexaphosphate) to inositol and inorganic phosphate. In the process, minerals that have been complexed with phytate are released.

Phytate occurs as a source of stored phosphorous in virtually all plant feeds (Phytic Acid, Chemistry and Applications, E. Graf (Ed.), Pilatus Press: Minneapolis, MN, U.S.A., 1986). Phytic acid forms a normal part of the seed in cereals and legumes. It functions to bind dietary minerals that are essential to the new plant as it emerges from the seed. When the phosphate groups of phytic acid are removed by the seed enzyme phytase, the ability to bind metal ions is lost and the minerals become available to the plant. In livestock feed grains, the trace minerals bound by phytic acid are only partially available for absorption by monogastric animals, which lack phytase activity. Although some hydrolysis of phytate occurs in the colon, most phytate passes through the gastrointestinal tract of monogastric animals and is excreted in the manure contributing

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to fecal phosphate pollution problems in areas of intense livestock production. Inorganic phosphorous released in the colon has no nutritional value to livestock because inorganic phosphorous is absorbed only in the small intestine. Thus, a significant amount of the nutritionally important dietary minerals are potentially not available to monogastric animals.

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Conversion of phytate to inositol and inorganic phosphorous can be catalyzed by microbial enzymes referred to broadly as phytases. Phytases such as phytase #EC 3.1.3.8 are capable of catalyzing hydrolysis of myo-inositol hexaphosphate to D-myo-inositol 1,2,4,5,6-pentaphosphate and orthophosphate. Certain fungal phytases reportedly hydrolyze inositol pentaphosphate to tetra-, tri-, and lower phosphates; e.g., *A. ficuum* phytases reportedly produce mixtures of myoinositol di- and mono-phosphate (Ullah, 1988). Phytase producing microorganisms comprise bacteria such as *Bacillus subtilis* (V.K. Powar and V.J. Jagannathan, *J. Bacteriol.* 151:1102-1108, 1982) and *Pseudomonas* (D.J. Cosgrove, *Austral. J. Biol. Sci.* 2:1207-1220, 1970); yeasts such as *Saccharomyces cerevisiae* (N.R. Nayini and P. Markakis, *Lebensmittel Wissenschaft und Technologie* 17:24-26, 1984); and fungi such as *Aspergillus terreus* (K. Yamada, et al., *Agric. Biol. Chem.* 32:1275-1282, 1968). The possible use of microbes capable of producing phytase as a feed additive for monogastric animals has been reported previously (Shieh and Ware, U.S. Patent No. 3,297,548; Nelson, T.S. et al., *J. Nutrition* 101:1289-1294, 1971).

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Microbial phytases may also reportedly be useful for producing animal feed from certain industrial processes, e.g., wheat and corn waste products. The wet milling process of corn produces glutens sold as animal feeds. Addition of phytase may reportedly improve the nutritional value of the feed product. Fungal phytase enzymes and process conditions (t~50°C and pH ~5.5) have been reported previously in European Patent Application 0 321 004. In processing soybean meal the presence of phytate reportedly renders the meal and wastes unsuitable for feeds used in rearing fish, poultry and other non-ruminants as well as calves fed on milk. Phytase is reportedly useful for improving the nutrient and

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commercial value of this high protein soy material (see Finase Enzymes by Alko, Rajamaki, Finland). A combination of phytase and a pH 2.5 optimum acid phosphatase form *A. niger* has been used by Alko, Ltd as an animal feed supplement in their phytic acid degradative product Finas F and Finase S. A cost-effective source of phytase would greatly enhance the value of soybean meals as an animal feed (Shieh et al., 1969).

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Phytase and less specific acid phosphatases are produced by the fungus *Aspergillus ficuum* as extracellular enzymes (Shieh et al., 1969). Ullah reportedly purified a phytase from wild-type *A. ficuum* that had an apparent molecular weight of 61.7 kDa (on SDS-PAGE; as corrected for glycosylation); pH optima at pH 2.5 and pH 5.5; a Km of about 40(m; and, a specific activity of about 50U/mg (Ullah, A., Preparative Biochem 18:443-458, 1988); PCT patent application WO 91/05053 also reportedly discloses isolation and molecular cloning of a phytase from *Aspergillus ficuum* with pH optima at pH 2.5 and pH 5.5, a Km of about 250(m, and specific activity of about 100U/mg protein.

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Acid phosphatases are enzymes that catalytically hydrolyze a wide variety of phosphate esters and usually exhibit pH optima below 6.0 (Hollander, 1971); e.g., #EC 3.1.3.2 catalyzes hydrolysis of orthophosphoric monoesters to orthophosphate products. An acid phosphatase has reportedly been purified from *A. ficuum*. The deglycosylated form of the acid phosphatase has an apparent molecular weight of 32.6 kDa (Ullah et al., 1987).

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The object of the present invention provides a recombinant phytase isolated from *Escherichia coli* B that improves the efficiency of release of phosphorous from phytate and the salts of phytic acid. Another object of the present invention provides a source of a recombinant enzyme that is suitable for commercial use in feeds and industrial processes with minimal processing.

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Summary of the Invention

The present invention provides a polynucleotide and a polypeptide encoded thereby which has been identified as a phytase enzyme having phytase activity. In accordance with one aspect of the present invention, there is provided a novel recombinant enzyme, as well as active fragments, analogs and derivatives thereof.

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In accordance with another aspect of the present invention, there are provided isolated nucleic acid molecules encoding the enzyme of the present invention including mRNA, DNA, cDNA, genomic DNA as well as active analogs and fragments of such enzyme.

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In accordance with yet a further aspect of the present invention, there is provided a process for producing such polypeptide by recombinant techniques comprising culturing recombinant prokaryotic and/or eukaryotic host cells, containing a nucleic acid sequence encoding an enzyme of the present invention, under conditions promoting expression of said enzyme and subsequent recovery of said enzyme.

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In accordance with yet a further aspect of the present invention, there is provided a process for utilizing such enzyme, or polynucleotide encoding such enzymes for use in commercial processes, such as, for example, processes that liberate minerals from phytates in plant materials either *in vitro*, i.e., in feed treatment processes, or *in vivo*, i.e., by administering the enzyme to animals.

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In accordance with yet a further aspect of the present invention, there is provided a process for utilizing such enzymes, or polynucleotides encoding such enzymes, for *in vitro* purposes related to scientific research, for example, to generate probes for identifying similar sequences which might encode similar enzymes from other organisms.

These and other aspects of the present invention should be apparent to those skilled in the art from the teachings herein.

**BRIEF DESCRIPTION OF THE DRAWINGS**

The following drawings are illustrative of embodiments of the invention and are not meant to limit the scope of the invention as encompassed by the claims.

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Figure 1 shows the nucleotide and deduced amino acid sequences the enzyme of the present invention. Sequencing was performed using a 378 automated DNA sequencer (Applied Biosystems, Inc.).

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Figure 2 shows the pH and temperature profile and stability data for the phytase enzyme of the present invention. The assay used for these analysis is the following for the detection of phytase activity: Phytase activity is measured by incubating 150(l of the enzyme preparation with 600(l of 2 mM sodium phytate in 100 mM Tris HCl buffer pH 7.5, supplemented with 1mM CaCl<sub>2</sub> for 30 minutes at 37(C. After incubation the reaction is stopped by adding 750(l of 5% trichloroacetic acid. Phosphate released was measured against phosphate standard spectrophotometrically at 700nm after adding 1500(l of the color reagent (4 volumes of 1.5% ammonium molybdate in 5.5% sulfuric acid and 1 volume of 2.7% ferrous sulfate; Shimizu, M., 1992; Biosci. Biotech. Biochem., 56:1266-1269). OD at 700nm is indicated on the Y-axis of the graphs in Figure 2. Temperature or pH is indicated on the X-axis of the graphs.

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DETAILED DESCRIPTION OF THE INVENTION

The term "gene" means the segment of DNA involved in producing a polypeptide chain; it includes regions preceding and following the coding region (leader and trailer) as well as intervening sequences (introns) between individual coding segments (exons).

5 A coding sequence is "operably linked to" another coding sequence when RNA polymerase will transcribe the two coding sequences into a single mRNA, which is then translated into a single polypeptide having amino acids derived from both coding sequences. The coding sequences need not be contiguous to one another so long as the expressed sequences are ultimately processed to produce the desired protein.

10 "Recombinant" enzymes refer to enzymes produced by recombinant DNA techniques; *i.e.*, produced from cells transformed by an exogenous DNA construct encoding the desired enzyme. "Synthetic" enzymes are those prepared by chemical synthesis.

15 A DNA "coding sequence of" or a "nucleotide sequence encoding" a particular enzyme, is a DNA sequence which is transcribed and translated into an enzyme when placed under the control of appropriate regulatory sequences. A "promotor sequence" is a DNA regulatory region capable of binding RNA polymerase in a cell and initiating transcription of a downstream (3' direction) coding sequence. The promoter is part of the DNA sequence. This sequence region has a start codon at its 3' terminus. The promoter sequence does include the minimum number of bases where elements necessary 20 to initiate transcription at levels detectable above background. However, after the RNA polymerase binds the sequence and transcription is initiated at the start codon (3' terminus with a promoter), transcription proceeds downstream in the 3' direction. Within the promotor sequence will be found a transcription initiation site (conveniently defined by mapping with nuclease S1) as well as protein binding domains (consensus sequences) 25 responsible for the binding of RNA polymerase.

The present invention provides purified a recombinant enzyme that catalyzes the hydrolysis of phytate to inositol and free phosphate with release of minerals from the phytic acid complex. An exemplary purified enzyme is a phytase derived from *Escherichia coli* B. This exemplary enzyme is shown in Figure 1, SEQ ID NO:2.

5 The polynucleotide encoding SEQ ID NO:2 was originally recovered from genomic DNA isolated from *Escherichia coli* B as described below. It contains an open reading frame encoding a protein of 432 amino acid residues.

10 In one embodiment, the phytase enzyme of SEQ ID NO:2 of the present invention has a molecular weight of about 47,056 kilodaltons as measured by SDS-PAGE gel electrophoresis and an inferred molecular weight from the nucleotide sequence of the gene. The pI is 6.70. The pH and temperature profile and stability data for this enzyme is presented in Figure 2. This purified enzyme may be used to catalyze the hydrolysis of phytate to inositol and free phosphate where desired. The phytase enzyme of the present invention has a high thermostability.

15 In accordance with an aspect of the present invention, there are provided isolated nucleic acid molecules (polynucleotides) which encode for the mature enzyme having the deduced amino acid sequence of Figure 1.

20 This invention can be used to isolate nucleic acid sequences substantially similar to the isolated nucleic acid molecule encoding an phytase enzyme disclosed in Figure 1 (SEQ ID NO:1). Isolated nucleic acid sequences are substantially similar if: (i) they are capable of hybridizing under stringent conditions, hereinafter described, to SEQ ID NO:1; or (ii) they encode DNA sequences which are degenerate to SEQ ID NO:1. Degenerate DNA sequences encode the amino acid sequence of SEQ ID NO:2, but have variations in the nucleotide coding sequences. As used herein, "substantially similar" 25 refers to the sequences having similar identity to the sequences of the instant invention.

The nucleotide sequences that are substantially similar can be identified by hybridization or by sequence comparison. Enzyme sequences that are substantially similar can be identified by one or more of the following: proteolytic digestion, gel electrophoresis and/or microsequencing.

5 One means for isolating a nucleic acid molecule encoding a phytase enzyme is to probe a genomic gene library with a natural or artificially designed probe using art recognized procedures (see, for example: Current Protocols in Molecular Biology, Ausubel F.M. *et al.* (EDS.) Green Publishing Company Assoc. and John Wiley Interscience, New York, 1989, 1992). It is appreciated to one skilled in the art that SEQ ID NO:1, or fragments thereof (comprising at least 15 contiguous nucleotides), is a particularly useful probe. 10 Other particular useful probes for this purpose are hybridizable fragments to the sequences of SEQ ID NO:1 (comprising at least 10 contiguous nucleotides and at least 70% complementary to a target sequence), is a particularly useful probe. Other particular useful probes for this purpose are hybridizable fragments to the sequences of SEQ ID NO:1 (*i.e.*, comprising at least 10 contiguous nucleotides and at least 70% 15 complementary to a target sequence).

With respect to nucleic acid sequences which hybridize to specific nucleic acid sequences disclosed herein, hybridization may be carried out under conditions of reduced stringency, medium stringency or even stringent conditions. As an example of 20 oligonucleotide hybridization, a polymer membrane containing immobilized denatured nucleic acid is first prehybridized for 30 minutes at 45°C in a solution consisting of 0.9 M NaCl, 50 mM NaH<sub>2</sub>PO<sub>4</sub>, pH 7.0, 5.0 mM Na<sub>2</sub>EDTA, 0.5% SDS, 10X Denhardt's, and 0.5 mg/mL polyriboadenylic acid. Approximately 2 X 10<sup>7</sup> cpm (specific activity 4-9 X 10<sup>8</sup> cpm/ug) of <sup>32</sup>P end-labeled oligonucleotide probe are then added to the solution. 25 After 12-16 hours of incubation, the membrane is washed for 30 minutes at room temperature in 1X SET (150 mM NaCl, 20 mM Tris hydrochloride, pH 7.8, 1 mM Na<sub>2</sub>EDTA) containing 0.5% SDS, followed by a 30 minute wash in fresh 1X SET at

Tm-10(C for the oligo-nucleotide probe. The membrane is then exposed to auto-radiographic film for detection of hybridization signals.

Stringent conditions means hybridization will occur only if there is at least 90% identity, preferably at least 95% identity and most preferably at least 97% identity between the sequences. See J. Sambrook *et al.*, Molecular Cloning, A Laboratory Manual (2d Ed. 5 1989) (Cold Spring Harbor Laboratory) which is hereby incorporated by reference in its entirety.

"Identity" as the term is used herein, refers to a polynucleotide sequence which comprises a percentage of the same bases as a reference polynucleotide (SEQ ID NO:1). 10 For example, a polynucleotide which is at least 90% identical to a reference polynucleotide, has polynucleotide bases which are identical in 90% of the bases which make up the reference polynucleotide and may have different bases in 10% of the bases which comprise that polynucleotide sequence.

The present invention also relates to polynucleotides which differ from the reference 15 polynucleotide such that the changes are silent changes, for example the changes do not alter the amino acid sequence encoded by the polynucleotide. The present invention also relates to nucleotide changes which result in amino acid substitutions, additions, deletions, fusions and truncations in the enzyme encoded by the reference polynucleotide (SEQ ID NO:1). In a preferred aspect of the invention these enzymes retain the same 20 biological action as the enzyme encoded by the reference polynucleotide.

It is also appreciated that such probes can be and are preferably labeled with an 25 analytically detectable reagent to facilitate identification of the probe. Useful reagents include but are not limited to radioactivity, fluorescent dyes or enzymes capable of catalyzing the formation of a detectable product. The probes are thus useful to isolate complementary copies of DNA from other animal sources or to screen such sources for

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related sequences.

The present invention provides a substantially pure phytase enzyme. The term "substantially pure" is used herein to describe a molecule, such as a polypeptide (e.g., a phytase polypeptide, or a fragment thereof) that is substantially free of other 5 proteins, lipids, carbohydrates, nucleic acids, and other biological materials with which it is naturally associated. For example, a substantially pure molecule, such as a polypeptide, can be at least 60%, by dry weight, the molecule of interest. The purity of the polypeptides can be determined using standard methods including, e.g., polyacrylamide gel electrophoresis (e.g., SDS-PAGE), column chromatography (e.g., 10 high performance liquid chromatography (HPLC)), and amino-terminal amino acid sequence analysis.

The phytase polypeptide included in the invention can have the amino acid sequences of Phytase shown in Figure 1 (SEQ ID NO:1). Phytase polypeptides, such as those isolated from *E. coli* B, can be characterized by catalyzing the hydrolysis of phytate to inositol and free phosphate with the release of minerals from the phytic acid complex. 15

Also included in the invention are polypeptides having sequences that are "substantially identical" to the sequence of a phytase polypeptide, such as one of SEQ ID 1. A "substantially identical" amino acid sequence is a sequence that differs from a reference sequence only by conservative amino acid substitutions, for example, substitutions of one 20 amino acid for another of the same class (e.g., substitution of one hydrophobic amino acid, such as isoleucine, valine, leucine, or methionine, for another, or substitution of one polar amino acid for another, such as substitution of arginine for lysine, glutamic acid for aspartic acid, or glutamine for asparagine).

Fragments of the phytase polypeptide of the present invention can retain at least one 25 phytase-specific activity or epitope. Phytase activity can be assayed by examining the

catalysis of phytate to inositol and free phosphate. For example, a phytase polypeptide fragment containing, *e.g.*, at least 8-10 amino acids can be used as an immunogen in the production of phytase-specific antibodies. The fragment can contain, for example, an amino acid sequence that is conserved in phytases, and this amino acid sequence can contain amino acids that are conserved in phytases. Such fragments can easily be identified by comparing the sequences of phytases found in Figure 1. In addition to their use as peptide immunogens, the above-described phytase fragments can be used in immunoassays, such as ELISAs, to detect the presence of phytase-specific antibodies in samples.

Other phytase polypeptides included in the invention are polypeptides having amino acid sequences that are at least 50% identical to the amino acid sequence of a phytase polypeptide, such as SEQ ID NO:2. The length of comparison in determining amino acid sequence homology can be, for example, at least 15 amino acids, for example, at least 20, 25, or 35 amino acids. Homology can be measured using standard sequence analysis software (*e.g.*, Sequence Analysis Software Package of the Genetics Computer Group, University of Wisconsin Biotechnology Center, 1710 University Avenue, Madison, WI 53705; also see Ausubel, *et al.*, *supra*). Such procedures and algorithms include, for example, a BLAST program (Basic Local Alignment Search Tool at the National Center for Biological Information), ALIGN, AMAS (Analysis of Multiply Aligned Sequences), AMPS (Protein Multiple Sequence Alignment), ASSET (Aligned Segment Statistical Evaluation Tool), BANDS, BESTSCOR, BIOSCAN (Biological Sequence Comparative Analysis Node), BLIMPS (BLocks IMProved Searcher), FASTA, Intervals & Points, BMB, CLUSTAL V, CLUSTAL W, CONSENSUS, LCONSENSUS, WCONSENSUS, Smith-Waterman algorithm, DARWIN, Las Vegas algorithm, FNAT (Forced Nucleotide Alignment Tool), Framealign, Framesearch, DYNAMIC, FILTER, FSAP (Fristensky Sequence Analysis Package), GAP (Global Alignment Program), GENAL, GIBBS, GenQuest, ISSC (Sensitive Sequence Comparison), LALIGN (Local Sequence Alignment), LCP (Local Content Program), MACAW (Multiple Alignment

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Construction & Analysis Workbench), MAP (Multiple Alignment Program), MBLKP, MBLKN, PIMA (Pattern-Induced Multi-sequence Alignment), SAGA (Sequence Alignmnet by Genetic ALgorithm) and WHAT-IF.

5 The phytase polypeptide of the invention can be obtained using any of several standard methods. For example, phytase polypeptides can be produced in a standard recombinant expression systems (see below), chemically synthesized (this approach may be limited to small phytase peptide fragments), or purified from organisms in which they are naturally expressed.

10 The invention also provides isolated nucleic acid molecules that encode the phytase polypeptide described above. For example, nucleic acids that encode SEQ ID NO:1 are included in the invention. These nucleic acids can contain naturally occurring nucleotide sequences, or sequences that differ from those of the naturally occurring nucleic acids that encode phytases, but encode the same amino acids, due to the degeneracy of the genetic code. The nucleic acids of the invention can contain DNA or RNA nucleotides, 15 or combinations or modifications thereof. Exemplary nucleic acids of the invention are shown in SEQ ID NO:1.

20 By "isolated nucleic acid" is meant a nucleic acid, *e.g.*, a DNA or RNA molecule, that is not immediately contiguous with the 5' and 3' flanking sequences with which it normally is immediately contiguous when present in the naturally occurring genome of the organism from which it is derived. The term thus describes, for example, a nucleic acid that is incorporated into a vector, such as a plasmid or viral vector; a nucleic acid that is incorporated into the genome of a heterologous cell (or the genome of a homologous cell, but at a site different from that at which it naturally occurs); and a nucleic acid that exists as a separate molecule, *e.g.*, a DNA fragment produced by PCR 25 amplification or restriction enzyme digestion, or an RNA molecule produced by *in vitro* transcription. The term also describes a recombinant nucleic acid that forms part of a

hybrid gene encoding additional polypeptide sequences that can be used, for example, in the production of a fusion protein.

The nucleic acid molecules of the invention can be used as templates in standard methods for production of phytase gene products (e.g., phytase RNAs and phytase polypeptides).  
5 In addition, the nucleic acid molecules that encode phytase polypeptides (and fragments thereof) and related nucleic acids, such as (1) nucleic acids containing sequences that are complementary to, or that hybridize to, nucleic acids encoding phytase polypeptides, or fragments thereof (e.g., fragments containing at least 10, 12, 15, 20, or 25 nucleotides); and (2) nucleic acids containing sequences that hybridize to sequences that are complementary to nucleic acids encoding phytase polypeptides, or fragments thereof (e.g., fragments containing at least 10, 12, 15, 20, or 25 nucleotides); can be used in methods focused on their hybridization properties. For example, as is described in further detail below, such nucleic acid molecules can be used in the following methods: PCR methods for synthesizing phytase nucleic acids, methods for detecting the presence of a phytase nucleic acid in a sample, screening methods for identifying nucleic acids encoding new phytase family members. Oligonucleotide probes useful for screening methods are from 10 to about 150 nucleotides in length. Further, such probes are preferably 10 to about 100 nucleotides in length and more preferably from 10 to about 15  
10 15 50 nucleotides in length.

20 The invention also includes methods for identifying nucleic acid molecules that encode members of the phytase polypeptide family in addition to SEQ ID NO:1. In these methods, a sample, e.g., a nucleic acid library, such as a cDNA library, that contains a nucleic acid encoding a phytase polypeptide is screened with a phytase-specific probe, e.g., a phytase-specific nucleic acid probe. Phytase-specific nucleic acid probes are nucleic acid molecules (e.g., molecules containing DNA or RNA nucleotides, or combinations or modifications thereof) that specifically hybridize to nucleic acids encoding phytase polypeptides, or to complementary sequences thereof. The term  
25

"phytase-specific probe," in the context of this method of invention, refers to probes that bind to nucleic acids encoding phytase polypeptides, or to complementary sequences thereof, to a detectably greater extent than to nucleic acids encoding other enzymes, or to complementary sequences thereof.

5 The invention facilitates production of phytase-specific nucleic acid probes. Methods for obtaining such probes can be designed based on the amino acid sequences shown in Figure 1. The probes, which can contain at least 10, e.g., at least 15, 25, 35, 50, 100, or 10 150 nucleotides, can be produced using any of several standard methods (see, e.g., Ausubel, *et al.*, *supra*). For example, preferably, the probes are generated using PCR amplification methods. In these methods, primers are designed that correspond to phytase-conserved sequences (see Figure 1), which can include phytase-specific amino acids, and the resulting PCR product is used as a probe to screen a nucleic acid library, such as a cDNA library.

15 The coding sequences for the phytase enzymes of the present invention were identified by preparing *E.coli* B genomic DNA, for example, and recovering (via, for example, PCR amplification) from the genomic DNA, DNA encoding phytase activity. Such methods for recovery are well-known in the art. One means, for example, comprises 20 designing amplification primers to recover the coding sequence, amplifying the gene from the genomic DNA, subcloning the DNA into a vector, transforming the resulting construct into a host strain, and expressing the phytase enzyme for evaluation. Such procedures are well known in the art and methods are provided, for example, in Maniatis, T., *et al.*, Molecular Cloning, Cold Spring Harbor Press, New York, 1982, 25 which is hereby incorporated by reference in its entirety.

25 In a preferred embodiment, the enzyme of the present invention, was isolated from an *E.coli* B genomic DNA by the following technique:

*E.coli* B genomic DNA was obtained from Sigma (Catalog # D-2001), St. Louis, New

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Jersey.

The following primers were used to amplify the gene directly from the genomic DNA:

5' primer      gtttctgaattcaaggaggaattaaATGAAAGCGATCTTAATCCCATT

3' primer      gtttctggatccTTACAAACTGCACGCCGGTAT

5      Pfu polymerase was used according to manufacturers protocol (Stratagene Cloning Systems, Inc., La Jolla, CA).

PCR product and pQE60 vector (Qiagen) were both digested with EcoRI and BglII restriction endonucleases (New England Biolabs) according to manufacturers protocols. Ligation and transformation into, and expression in M15 pREP4 host cells (Qiagen) yields c-term 6X-His tagged protein.

10      Fragments of the full length gene of the present invention may be used as a hybridization probe for a cDNA or a genomic library to isolate the full length DNA and to isolate other DNAs which have a high sequence similarity to the gene or similar biological activity. Probes of this type have at least 10, preferably at least 15, and even more preferably at least 30 bases and may contain, for example, at least 50 or more bases. The probe may 15 also be used to identify a DNA clone corresponding to a full length transcript and a genomic clone or clones that contain the complete gene including regulatory and promotor regions, exons, and introns.

20      The isolated nucleic acid sequences and other enzymes may then be measured for retention of biological activity characteristic to the enzyme of the present invention, for example, in an assay for detecting enzymatic phytase activity. Such enzymes include truncated forms of phytase, and variants such as deletion and insertion variants.

25      Examples of such assays include the following assay for the detection of phytase activity: Phytase activity can be measured by incubating 150 $\mu$ l of the enzyme preparation with 600 $\mu$ l of 2 mM sodium phytate in 100 mM Tris HCl buffer pH 7.5, supplemented with

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1mM CaCl<sub>2</sub> for 30 minutes at 37(C. After incubation the reaction is stopped by adding 750(l of 5% trichloroacetic acid. Phosphate released was measured against phosphate standard spectrophotometrically at 700nm after adding 1500(l of the color reagent (4 volumes of 1.5% ammonium molybdate in 5.5% sulfuric acid and 1 volume of 2.7% ferrous sulfate; Shimizu, M., 1992; Biosci. Biotech. Biochem., 56:1266-1269). One unit of enzyme activity is defined as the amount of enzyme required to liberate one (mol Pi per min under assay conditions. Specific activity can be expressed in units of enzyme activity per mg of protein.

The enzyme of the present invention has enzymatic activity with respect to the hydrolysis of phytate to inositol and free phosphate.

The polynucleotide of the present invention may be in the form of DNA which DNA includes cDNA, genomic DNA, and synthetic DNA. The DNA may be double-stranded or single-stranded, and if single stranded may be the coding strand or non-coding (anti-sense) strand. The coding sequence which encodes the mature enzyme may be identical to the coding sequences shown in Figure 1 and/or that of the deposited clone (SEQ ID NO:1), or may be a different coding sequence which coding sequence, as a result of the redundancy or degeneracy of the genetic code, encodes the same mature enzyme as the DNA of Figure 1 (e.g., SEQ ID NO:1).

The polynucleotide which encodes for the mature enzyme of Figure 1 (e.g., SEQ ID NO:2) may include, but is not limited to: only the coding sequence for the mature enzyme; the coding sequence for the mature enzyme and additional coding sequence such as a leader sequence or a proprotein sequence; the coding sequence for the mature enzyme (and optionally additional coding sequence) and non-coding sequence, such as introns or non-coding sequence 5' and/or 3' of the coding sequence for the mature enzyme.

Thus, the term "polynucleotide encoding an enzyme (protein)" encompasses a polynucleotide which includes only coding sequence for the enzyme as well as a polynucleotide which includes additional coding and/or non-coding sequence.

5 The present invention further relates to variants of the hereinabove described polynucleotides which encode for analogs and derivatives of the enzyme having the deduced amino acid sequence of Figure 1 (e.g., SEQ ID NO:2). The variant of the polynucleotide may be a naturally occurring allelic variant of the polynucleotide or a non-naturally occurring variant of the polynucleotide.

10 Thus, the present invention includes polynucleotides encoding the same mature enzyme as shown in Figure 1 as well as variants of such polynucleotides which variants encode for a derivative or analog of the enzyme of Figure 1. Such nucleotide variants include deletion variants, substitution variants and addition or insertion variants.

15 As hereinabove indicated, the polynucleotide may have a coding sequence which is a naturally occurring allelic variant of the coding sequence shown in Figure 1. As known in the art, an allelic variant is an alternate form of a polynucleotide sequence which may have a substitution, deletion or addition of one or more nucleotides, which does not substantially alter the function of the encoded enzyme.

20 The present invention also includes polynucleotides, wherein the coding sequence for the mature enzyme may be fused in the same reading frame to a polynucleotide sequence which aids in expression and secretion of an enzyme from a host cell, for example, a leader sequence which functions to control transport of an enzyme from the cell. The enzyme having a leader sequence is a preprotein and may have the leader sequence cleaved by the host cell to form the mature form of the enzyme. The polynucleotides may also encode for a proprotein which is the mature protein plus additional 5' amino acid residues. A mature protein having a prosequence is a proprotein and is an inactive

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form of the protein. Once the prosequence is cleaved an active mature protein remains.

Thus, for example, the polynucleotide of the present invention may encode for a mature enzyme, or for an enzyme having a prosequence or for an enzyme having both a prosequence and a presequence (leader sequence).

5 The present invention further relates to a enzyme which has the deduced amino acid sequence of Figure 1, as well as analogs and derivatives of such enzyme.

10 The terms "derivative" and "analog" when referring to the enzyme of Figure 1 means a enzyme which retains essentially the same biological function or activity as such enzyme. Thus, an analog includes a proprotein which can be activated by cleavage of the proprotein portion to produce an active mature enzyme.

15 The enzyme of the present invention may be a recombinant enzyme, a natural enzyme or a synthetic enzyme, preferably a recombinant enzyme.

20 The derivative or analog of the enzyme of Figure 1 may be (i) one in which one or more of the amino acid residues are substituted with an amino acid residue which is not encoded by the genetic code, or (ii) one in which one or more of the amino acid residues includes a substituent group, or (iii) one in which the mature enzyme is fused with another compound, such as a compound to increase the half-life of the enzyme (for example, polyethylene glycol), or (iv) one in which the additional amino acids are fused to the mature enzyme, such as a leader or secretory sequence or a sequence which is employed for purification of the mature enzyme or a proprotein sequence. Such derivatives and analogs are deemed to be within the scope of those skilled in the art from the teachings herein.

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The enzymes and polynucleotides of the present invention are preferably provided in an isolated form, and preferably are purified to homogeneity.

The term "isolated" means that the material is removed from its original environment (e.g., the natural environment if it is naturally occurring). For example, a naturally-occurring polynucleotide or enzyme present in a living animal is not isolated, but the same polynucleotide or enzyme, separated from some or all of the coexisting materials in the natural system, is isolated. Such polynucleotides could be part of a vector and/or such polynucleotides or enzymes could be part of a composition, and still be isolated in that such vector or composition is not part of its natural environment.

10 The enzymes of the present invention includes an enzyme of Figure 1 (in particular the mature enzyme) as well as enzymes which have at least 70% similarity (preferably at least 70% identity) to an enzyme of Figure 1 and more preferably at least 90% similarity (more preferably at least 90% identity) to an enzyme of Figure 1 and still more preferably at least 95% similarity (still more preferably at least 95% identity) to an enzyme of Figure 1 and also include portions of such enzymes with such portion of the enzyme 15 generally containing at least 30 amino acids and more preferably at least 50 amino acids.

20 As known in the art "similarity" between two enzymes is determined by comparing the amino acid sequence and its conserved amino acid substitutes of one enzyme to the sequence of a second enzyme. Similarity in nucleic acid and amino acid sequences may be determined by procedures and algorithms which are well-known in the art. Such 25 procedures and algorithms include, for example, a BLAST program (Basic Local Alignment Search Tool at the National Center for Biological Information), ALIGN, AMAS (Analysis of Multiply Aligned Sequences), AMPS (Protein Multiple Sequence Alignment), ASSET (Aligned Segment Statistical Evaluation Tool), BANDS, BESTSCOR, BIOSCAN (Biological Sequence Comparative Analysis Node), BLIMPS (BLocks IMProved Searcher), FASTA, Intervals & Points, BMB, CLUSTAL V,

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CLUSTAL W, CONSENSUS, LCONSENSUS, WCONSENSUS, Smith-Waterman algorithm, DARWIN, Las Vegas algorithm, FNAT (Forced Nucleotide Alignment Tool), Framealign, Framesearch, DYNAMIC, FILTER, FSAP (Fristensky Sequence Analysis Package), GAP (Global Alignment Program), GENAL, GIBBS, GenQuest, ISSC (Sensitive Sequence Comparison), LALIGN (Local Sequence Alignment), LCP (Local Content Program), MACAW (Multiple Alignment Construction & Analysis Workbench), MAP (Multiple Alignment Program), MBLKP, MBLKN, PIMA (Pattern-Induced Multi-sequence Alignment), SAGA (Sequence Alignmnet by Genetic ALgorithm) and WHAT-IF.

A variant, i.e. a "analog" or "derivative" enzyme, and reference enzyme may differ in amino acid sequence by one or more substitutions, additions, deletions, fusions and truncations, which may be present in any combination.

Among preferred variants are those that vary from a reference by conservative amino acid substitutions. Such substitutions are those that substitute a given amino acid in a polypeptide by another amino acid of like characteristics. Typically seen as conservative substitutions are the replacements, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile; interchange of the hydroxyl residues Ser and Thr, exchange of the acidic residues Asp and Glu, substitution between the amide residues Asn and Gln, exchange of the basic residues Lys and Arg and replacements among the aromatic residues Phe, Tyr.

Most highly preferred are variants which retain the same biological function and activity as the reference polypeptide from which it varies.

Fragments or portions of the enzymes of the present invention may be employed for producing the corresponding full-length enzyme by peptide synthesis; therefore, the fragments may be employed as intermediates for producing the full-length enzymes. Fragments or portions of the polynucleotides of the present invention may be used to

synthesize full-length polynucleotides of the present invention.

The present invention also relates to vectors which include polynucleotides of the present invention, host cells which are genetically engineered with vectors of the invention and the production of enzymes of the invention by recombinant techniques.

5 Host cells are genetically engineered (transduced or transformed or transfected) with the vectors containing the polynucleotides of this invention. Such vectors may be, for example, a cloning vector or an expression vector. The vector may be, for example, in the form of a plasmid, a viral particle, a phage, etc. The engineered host cells can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transformants or amplifying the genes of the present invention. The culture conditions, such as temperature, pH and the like, are those previously used with the host cell selected for expression, and will be apparent to the ordinarily skilled artisan.

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15 The polynucleotides of the present invention may be employed for producing enzymes by recombinant techniques. Thus, for example, the polynucleotide may be included in any one of a variety of expression vectors for expressing an enzyme. Such vectors include chromosomal, nonchromosomal and synthetic DNA sequences, e.g., derivatives of SV40; bacterial plasmids; phage DNA; baculovirus; yeast plasmids; vectors derived from combinations of plasmids and phage DNA, viral DNA such as vaccinia, adenovirus, fowl pox virus, and pseudorabies. However, any other vector may be used as long as it is replicable and viable in the host.

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The appropriate DNA sequence may be inserted into the vector by a variety of procedures. In general, the DNA sequence is inserted into an appropriate restriction endonuclease site(s) by procedures known in the art. Such procedures and others are deemed to be within the scope of those skilled in the art.

5 The DNA sequence in the expression vector is operatively linked to an appropriate expression control sequence(s) (promoter) to direct mRNA synthesis. As representative examples of such promoters, there may be mentioned: LTR or SV40 promoter, the *E. coli*. *lac* or *trp*, the phage lambda  $P_L$  promoter and other promoters known to control expression of genes in prokaryotic or eukaryotic cells or their viruses. The expression vector also contains a ribosome binding site for translation initiation and a transcription terminator. The vector may also include appropriate sequences for amplifying expression.

10 In addition, the expression vectors preferably contain one or more selectable marker genes to provide a phenotypic trait for selection of transformed host cells such as dihydrofolate reductase or neomycin resistance for eukaryotic cell culture, or such as tetracycline or ampicillin resistance in *E. coli*.

15 The vector containing the appropriate DNA sequence as hereinabove described, as well as an appropriate promoter or control sequence, may be employed to transform an appropriate host to permit the host to express the protein.

20 As representative examples of appropriate hosts, there may be mentioned: bacterial cells, such as *E. coli*, *Streptomyces*, *Bacillus subtilis*; fungal cells, such as yeast; insect cells such as *Drosophila S2* and *Spodoptera Sf9*; animal cells such as CHO, COS or Bowes melanoma; adenoviruses; plant cells, etc. The selection of an appropriate host is deemed to be within the scope of those skilled in the art from the teachings herein.

25 More particularly, the present invention also includes recombinant constructs comprising one or more of the sequences as broadly described above. The constructs comprise a vector, such as a plasmid or viral vector, into which a sequence of the invention has been inserted, in a forward or reverse orientation. In a preferred aspect of this embodiment, the construct further comprises regulatory sequences, including, for example, a promoter,

5 operably linked to the sequence. Large numbers of suitable vectors and promoters are known to those of skill in the art, and are commercially available. The following vectors are provided by way of example; Bacterial: pQE70, pQE60, pQE-9 (Qiagen), pBluescript II (Stratagene); pTRC99a, pKK223-3, pDR540, pRIT2T (Pharmacia); Eukaryotic: pXT1, pSG5 (Stratagene) pSVK3, pBPV, pMSG, pSVLSV40 (Pharmacia). However, any other plasmid or vector may be used as long as they are replicable and viable in the host.

10 Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda P<sub>R</sub>, P<sub>L</sub> and trp. Eukaryotic promoters include CMV immediate early, 15 HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art.

15 In a further embodiment, the present invention relates to host cells containing the above-described constructs. The host cell can be a higher eukaryotic cell, such as a mammalian cell, or a lower eukaryotic cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the construct into the host cell can be effected by calcium phosphate transfection, DEAE-Dextran mediated transfection, 20 or electroporation (Davis, L., Dibner, M., Battey, I., *Basic Methods in Molecular Biology*, (1986)).

The constructs in host cells can be used in a conventional manner to produce the gene product encoded by the recombinant sequence. Alternatively, the enzymes of the invention can be synthetically produced by conventional peptide synthesizers.

Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells

under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook *et al.*, Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor, N.Y., (1989),  
5 the disclosure of which is hereby incorporated by reference.

Transcription of the DNA encoding the enzymes of the present invention by higher eukaryotes is increased by inserting an enhancer sequence into the vector. Enhancers are  
10 cis-acting elements of DNA, usually about from 10 to 300 bp that act on a promoter to increase its transcription. Examples include the SV40 enhancer on the late side of the replication origin bp 100 to 270, a cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers.

Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, e.g., the ampicillin  
15 resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK),  $\lambda$ -factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase  
20 with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated enzyme. Optionally, the heterologous sequence can encode a fusion enzyme including an N-terminal identification peptide imparting desired characteristics, e.g., stabilization or simplified purification of expressed recombinant product.

25 Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation

and termination signals in operable reading phase with a functional promoter. The vector will comprise one or more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may also be employed as a matter of choice.

As a representative but nonlimiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM1 (Promega Biotec, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed.

Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced by appropriate means (e.g., temperature shift or chemical induction) and cells are cultured for an additional period.

Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents, such methods are well known to those skilled in the art.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, Cell, 23:175 (1981), and other cell lines capable of expressing a compatible vector, for example, the C127, 3T3, CHO, HeLa and BHK cell lines. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and enhancer, and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements.

The enzyme can be recovered and purified from recombinant cell cultures by methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps.

The enzymes of the present invention may be a naturally purified product, or a product of chemical synthetic procedures, or produced by recombinant techniques from a prokaryotic or eukaryotic host (for example, by bacterial, yeast, higher plant, insect and mammalian cells in culture). Depending upon the host employed in a recombinant production procedure, the enzymes of the present invention may be glycosylated or may be non-glycosylated. Enzymes of the invention may or may not also include an initial methionine amino acid residue.

The enzyme of this invention may be employed for any purpose in which such enzyme activity is necessary or desired. In a preferred embodiment the enzyme is employed for

catalyzing the hydrolysis of phytate. The degradation of phytate may be used in animal feed.

In a preferred embodiment, the enzyme of the present invention is a phytase enzyme which is stable to heat and is heat resistant and catalyzes the enzymatic hydrolysis of phytate, *i.e.*, the enzyme is able to renature and regain activity after a brief (*i.e.*, 5 to 5 30 seconds), or longer period, for example, minutes or hours, exposure to temperatures of 50°C optimum above 50°C.

The enzymes, their fragments or other derivatives, or analogs thereof, or cells expressing them can be used as an immunogen to produce antibodies thereto. These antibodies can 10 be, for example, polyclonal or monoclonal antibodies. The present invention also includes chimeric, single chain, and humanized antibodies, as well as Fab fragments, or the product of an Fab expression library. Various procedures known in the art may be used for the production of such antibodies and fragments. 11

Antibodies generated against the enzymes corresponding to a sequence of the present 15 invention can be obtained by direct injection of the enzymes into an animal or by administering the enzymes to an animal, preferably a nonhuman. The antibody so obtained will then bind the enzymes itself. In this manner, even a sequence encoding only a fragment of the enzymes can be used to generate antibodies binding the whole native enzymes. Such antibodies can then be used to isolate the enzyme from cells 20 expressing that enzyme.

For preparation of monoclonal antibodies, any technique which provides antibodies produced by continuous cell line cultures can be used. Examples include the hybridoma technique (Kohler and Milstein, 1975, *Nature*, 256:495-497), the trioma technique, the human B-cell hybridoma technique (Kozbor et al., 1983, *Immunology Today* 4:72), and

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the EBV-hybridoma technique to produce human monoclonal antibodies (Cole, et al., 1985, in *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc., pp. 77-96).

5 Techniques described for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce single chain antibodies to immunogenic enzyme products of this invention. Also, transgenic mice may be used to express humanized antibodies to immunogenic enzyme products of this invention.

10 Antibodies generated against the enzyme of the present invention may be used in screening for similar enzymes from other organisms and samples. Such screening techniques are known in the art. Antibodies may also be employed as a probe to screen gene libraries generated from this or other organisms to identify this or cross reactive activities.

15 Isolation and purification of polypeptides produced in the systems described above can be carried out using conventional methods, appropriate for the particular system. For example, preparative chromatography and immunological separations employing antibodies, such as monoclonal or polyclonal antibodies, can be used.

20 The term "antibody," as used herein, refers to intact immunoglobulin molecules, as well as fragments of immunoglobulin molecules, such as Fab, Fab', (Fab')<sub>2</sub>, Fv, and SCA fragments, that are capable of binding to an epitope of an endoglucanase polypeptide. These antibody fragments, which retain some ability to selectively bind to the antigen (e.g., an endoglucanase antigen) of the antibody from which they are derived, can be made using well known methods in the art (see, e.g., Harlow and Lane, *supra*), and are described further, as follows.

(1) A Fab fragment consists of a monovalent antigen-binding fragment of an antibody molecule, and can be produced by digestion of a whole antibody molecule with the enzyme papain, to yield a fragment consisting of an intact light chain and a portion of a heavy chain.

5 (2) A Fab' fragment of an antibody molecule can be obtained by treating a whole antibody molecule with pepsin, followed by reduction, to yield a molecule consisting of an intact light chain and a portion of a heavy chain. Two Fab' fragments are obtained per antibody molecule treated in this manner.

10 (3) A (Fab')<sub>2</sub> fragment of an antibody can be obtained by treating a whole antibody molecule with the enzyme pepsin, without subsequent reduction. A (Fab')<sub>2</sub> fragment is a dimer of two Fab' fragments, held together by two disulfide bonds.

(4) An Fv fragment is defined as a genetically engineered fragment containing the variable region of a light chain and the variable region of a heavy chain expressed as two chains.

15 (5) A single chain antibody ("SCA") is a genetically engineered single chain molecule containing the variable region of a light chain and the variable region of a heavy chain, linked by a suitable, flexible polypeptide linker.

20 As used in this invention, the term "epitope" refers to an antigenic determinant on an antigen, such as a phytase polypeptide, to which the paratope of an antibody, such as an phytase-specific antibody, binds. Antigenic determinants usually consist of chemically active surface groupings of molecules, such as amino acids or sugar side chains, and can have specific three-dimensional structural characteristics, as well as specific charge characteristics.

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As is mentioned above, antigens that can be used in producing phytase-specific antibodies include phytase polypeptides, *e.g.*, any of the phytase shown in Figures 1 5 polypeptide fragments. The polypeptide or peptide used to immunize an animal can be obtained by standard recombinant, chemical synthetic, or purification methods. As is well known in the art, in order to increase immunogenicity, an antigen can be conjugated to a carrier protein. Commonly used carriers include keyhole limpet hemocyanin (KLH), thyroglobulin, bovine serum albumin (BSA), and tetanus toxoid. The coupled peptide is then used to immunize the animal (*e.g.*, a mouse, a rat, or a rabbit). In addition to such carriers, well known adjuvants can be administered with the antigen to facilitate 10 induction of a strong immune response.

Phytase-specific polyclonal and monoclonal antibodies can be purified, for example, by binding to, and elution from, a matrix containing a phytase polypeptide, *e.g.*, the phytase 15 polypeptide (or fragment thereof) to which the antibodies were raised. Additional methods for antibody purification and concentration are well known in the art and can be practiced with the phytase-specific antibodies of the invention (see, for example, C oligan, *et al.*, Unit 9, *Current Protocols in Immunology*, Wiley Interscience, 1994).

Anti-idiotype antibodies corresponding to phytase-specific antigens are also included in the invention, and can be produced using standard methods. These antibodies are raised to phytase-specific antibodies, and thus mimic phytase-specific epitopes.

20 The members of a pair of molecules (*e.g.*, an antibody-antigen pair or a nucleic acid pair) are said to "specifically bind" to each other if they bind to each other with greater affinity than to other, non-specific molecules. For example, an antibody raised against an antigen to which it binds more efficiently than to a non-specific protein can be described as specifically binding to the antigen. (Similarly, a nucleic acid probe can be described as 25 specifically binding to a nucleic acid target if it forms a specific duplex with the target by base pairing interactions (see above).)

The present invention is further described with reference to the following examples; however, it is to be understood that the present invention is not limited to such examples. All parts or amounts, unless otherwise specified, are by weight.

In one aspect of the invention, a method for producing an phytase enzyme, such as those shown in Figures 1, is provided. The method includes growing a host cell which contains a polynucleotide encoding the enzyme (e.g., SEQ ID NO: 1), under conditions which allow the expression of the nucleic acid, and isolating the enzyme encoded by the nucleic acid. Methods of culturing the host cell are described in the Examples and are known by those of skill in the art.

In another embodiment, the invention provides a method for catalyzing the hydrolysis of phytate to inositol and free phosphate with release of minerals from the phytic acid complex. The method includes contacting phytate with a degrading effective amount of an enzyme of the invention, such as the enzyme shown in SEQ ID NO:1. The term "degrading effective" amount refers to the amount of enzyme which is required to degrade at least 50% of the phytate, as compared to phytate not contacted with the enzyme. Preferably, at least 80% of the phytate is degraded.

In another embodiment, the invention provides a method for hydrolyzing phospho-mono-ester bonds in phosphate, the method including administering an effective amount of an enzyme of the invention (e.g., SEQ ID NO:1), to yield inositol and free phosphate. An "effective" amount refers to the amount of enzyme which is required to hydrolyze at least 50% of the phospho-mono-ester bonds, as compared to phytate not contacted with the enzyme. Preferably, at least 80% of the bonds are hydrolyzed.

In order to facilitate understanding of the following examples certain frequently occurring methods and/or terms will be described.

"Plasmids" are designated by a lower case p preceded and/or followed by capital letters and/or numbers. The starting plasmids herein are either commercially available, publicly available on an unrestricted basis, or can be constructed from available plasmids in accord with published procedures. In addition, equivalent plasmids to those described are known in the art and will be apparent to the ordinarily skilled artisan.

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"Digestion" of DNA refers to catalytic cleavage of the DNA with a restriction enzyme that acts only at certain sequences in the DNA. The various restriction enzymes used herein are commercially available and their reaction conditions, cofactors and other requirements were used as would be known to the ordinarily skilled artisan. For analytical purposes, typically 1  $\mu$ g of plasmid or DNA fragment is used with about 2 units of enzyme in about 20  $\mu$ l of buffer solution. For the purpose of isolating DNA fragments for plasmid construction, typically 5 to 50  $\mu$ g of DNA are digested with 20 to 250 units of enzyme in a larger volume. Appropriate buffers and substrate amounts for particular restriction enzymes are specified by the manufacturer. Incubation times of about 1 hour at 37°C are ordinarily used, but may vary in accordance with the supplier's instructions. After digestion the reaction is electrophoresed directly on a polyacrylamide gel to isolate the desired fragment.

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Size separation of the cleaved fragments is generally performed using 8 percent polyacrylamide gel described by Goeddel, D. *et al.*, Nucleic Acids Res., 8:4057 (1980), for example.

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"Oligonucleotides" refers to either a single stranded polydeoxynucleotide or two complementary polydeoxynucleotide strands which may be chemically synthesized. Such synthetic oligonucleotides may or may not have a 5' phosphate. Those that do not will not ligate to another oligonucleotide without adding a phosphate with an ATP in the presence of a kinase. A synthetic oligonucleotide will ligate to a fragment that has not been dephosphorylated.

"Ligation" refers to the process of forming phosphodiester bonds between two double

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stranded nucleic acid fragments (Maniatis, T., et al., *Id.*, p. 146). Unless otherwise provided, ligation may be accomplished using known buffers and conditions with 10 units of T4 DNA ligase ("ligase") per 0.5 (g of approximately equimolar amounts of the DNA fragments to be ligated.

5 Unless otherwise stated, transformation was performed as described in the method of Sambrook, Fritsch and Maniatis, 1989. The following examples are intended to illustrate, but not to limit, the invention. While the procedures described in the examples are typical of those that can be used to carry out certain aspects of the invention, other procedures known to those skilled in the art can also be used. The following materials and methods were used in carrying out the experiments described in the examples.

10

**Example 1**

**Isolation, Bacterial Expression and Purification of Phytase**

15 *E. coli* B genomic DNA was obtained from Sigma (Catalog # D-2001), St. Louis, New Jersey.

The following primers were used to PCR amplify the gene directly from the genomic DNA:

5' primer        gtttctgaattcaaggaggaaatttaaATGAAAGCGATCTTAATCCCATT  
3' primer        gtttctggatccTTACAAACTGCACGCCGGTAT

20 Pfu polymerase in the PCR reaction, and amplification was performed according to manufacturers protocol (Stratagene Cloning Systems, Inc., La Jolla, CA).

PCR product was purified and purified product and pQE60 vector (Qiagen) were both digested with EcoRI and BglII restriction endonucleases (New England Biolabs) according to manufacturers protocols. Overnight ligations were performed using

standard protocols to yield pQE60.

The amplified sequences were inserted in frame with the sequence encoding for the RBS. The ligation mixture was then used to transform the *E. coli* strain M15/pREP4 (Qiagen, Inc.) by electroporation. M15/pREP4 contains multiple copies of the plasmid pREP4, which expresses the lacI repressor and also confers kanamycin resistance (Kan<sup>r</sup>). Plasmid DNA was isolated and confirmed by restriction analysis. Clones containing the desired constructs were grown overnight (O/N) in liquid culture in LB media supplemented with both Amp (100 ug/ml) and Kan (25 ug/ml). The O/N culture was used to inoculate a large culture at a ratio of 1:100 to 1:250. The cells were grown to an optical density 600 (O.D.<sup>600</sup>) of between 0.4 and 0.6. IPTG ("Isopropyl-B-D-thiogalacto pyranoside") was then added to a final concentration of 1 mM. IPTG induces by inactivating the lacI repressor, clearing the P/O leading to increased gene expression. Cells were grown an extra 3 to 4 hours. Cells were then harvested by centrifugation.

The primer sequences set out above may also be employed to isolate the target gene from the deposited material by hybridization techniques described above.

Numerous modifications and variations of the present invention are possible in light of the above teachings and, therefore, within the scope of the appended claims, the invention may be practiced otherwise than as particularly described. It is to be understood that, while the invention has been described with reference to the above detailed description, the foregoing description is intended to illustrate, but not to limit, the scope of the invention. Other aspects, advantages, and modifications of the invention are within the scope of the following claims. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety.

**What Is Claimed Is:**

1. Substantially pure phytase having an amino acid sequence selected from the group consisting of SEQ ID NO:2.
2. An isolated polynucleotide sequence encoding a phytase of claim 1.
3. An isolated polynucleotide selected from the group consisting of:
  - a) SEQ ID NO:1;
  - b) SEQ ID NO:1 wherein T can also be U;
4. The polynucleotide of claim 2, wherein the polynucleotide is isolated from a prokaryote.
5. An expression vector including the polynucleotide of claim 2.
6. The vector of claim 5, wherein the vector is a plasmid.
7. The vector of claim 5, wherein the vector is a virus-derived.
8. A host cell transformed with the vector of claim 5.
9. The host cell of claim 8, wherein the cell is prokaryotic.
10. Antibodies that bind to the polypeptide of claim 1.
11. The antibodies of claim 10, wherein the antibodies are polyclonal.

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12. The antibodies of claim 10, wherein the antibodies are monoclonal.
13. A method for producing an enzyme comprising growing a host cell of claim 8 under conditions which allow the expression of the nucleic acid and isolating the enzyme encoded by the nucleic acid.
14. A method for degrading phytase comprising contacting phytate with a degrading effective amount of the enzyme of claim 1.
15. A method for hydrolyzing the phospho-mono-ester bond in phytate comprising contacting an effective amount of the enzyme of claim 1 with phytate to hydrolyze the bond.
16. An animal feed composition comprising a phytase.
17. The composition of claim 16, wherein the phytase has an amino acid sequence as set forth in SEQ ID NO:2.
18. An isolated polynucleotide having at least 70% identity to a member selected from the group consisting of:
  - a) a polynucleotide encoding an enzyme comprising an amino acid sequence as set forth in SEQ ID NO:2;
  - b) a polynucleotide which is complementary to the polynucleotide of a); and
  - c) a polynucleotide comprising at least 15 bases of the polynucleotide of a) or b).
19. An oligonucleotide probe that hybridizes to a nucleic acid target region corresponding to a region selected from the nucleic acid sequence set forth in SEQ ID NO:1
20. The probe of claim 19, wherein the probe is from 10 to about 150 nucleotides in length.

21. The probe of claim 19, wherein the probe is from 10 to about 100 nucleotides in length.
22. The probe of claim 19, wherein the probe is from 10 to about 50 nucleotides in length.
23. The probe of claim 19, wherein the probe is from 10 to about 30 nucleotides in length.
24. The probe of claim 19, wherein the probe is from 10 to about 15 nucleotides in length.
25. The oligonucleotide probe of claim 19, wherein the probe comprises a segment of 10 contiguous bases which is at least 70% complementary to a target sequence of 10 contiguous nucleotides present in the target region.
26. The probe of claim 19, wherein the probe is detectably labeled.
27. The probe of claim 26, wherein the detectable label is selected from the group consisting of a radioisotope, a fluorescent compound, a bioluminescent compound, a chemiluminescent compound, a metal chelator or an enzyme.
28. The antibody of claim 10, wherein the antibody is detectably labeled.
29. An enzyme selected from the group consisting of:
  - a) an enzyme comprising an amino acid sequence which is at least 70% identical to the amino acid sequence set forth in SEQ ID NO:2; and
  - b) an enzyme which comprises at least 30 consecutive amino acid residues homologous with an enzyme of a).

(SEQ ID NO:1-nucleotide sequence and SEQ ID NO:2-amino acid sequence)

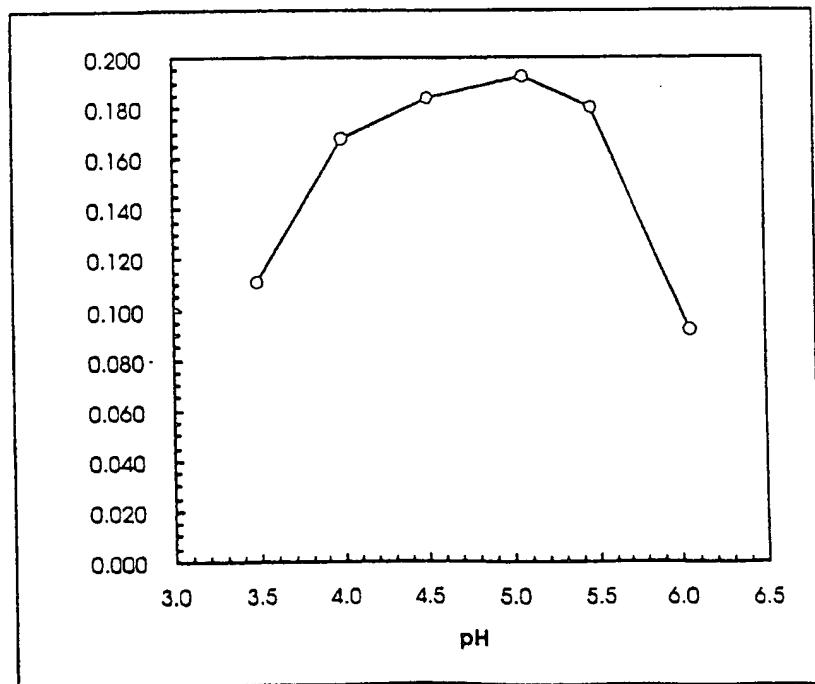
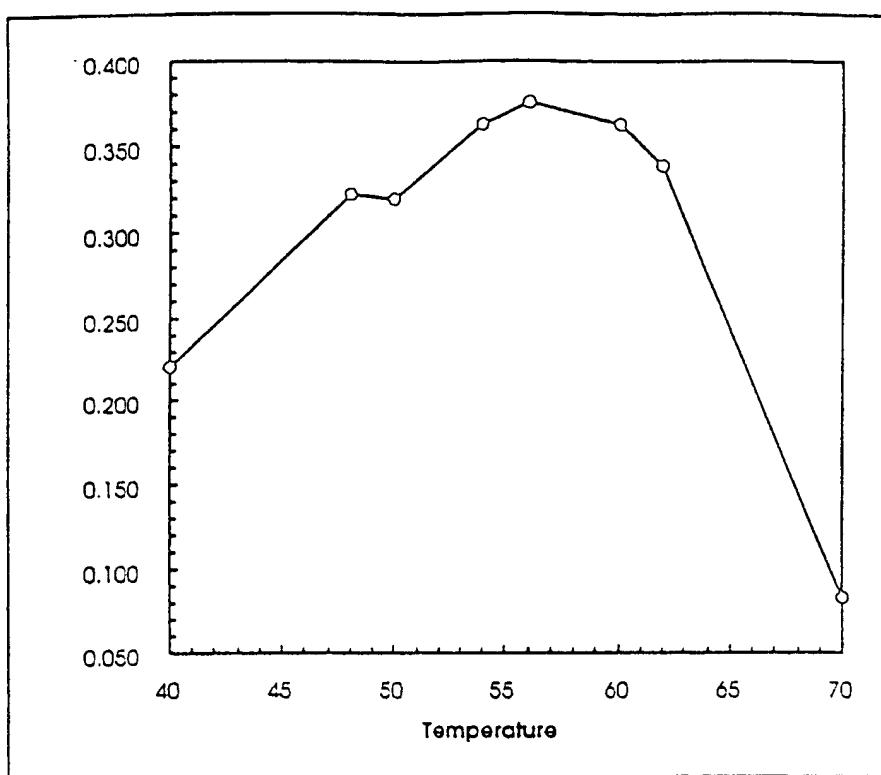
*Escherichia coli* B Phytase Sequence

1  
ATG AAA GCG ATC TTA ATC CCA TTT TTA TCT CTT CTG ATT CCG TTA ACC CCG  
Met Lys Ala Ile Leu Ile Pro Phe Leu Ser Leu Leu Ile Pro Leu Thr Pro  
CAA TCT GCA TTC GCT CAG AGT GAG CCG GAG CTG AAG CTG GAA AGT GTG GTG  
Gln Ser Ala Phe Ala Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser Val Val  
ATT GTC AGT CGT CAT GGT GTG CGT GCT CCA ACC AAG GCC ACG CAA CTG ATG  
Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr Gln Leu Met  
CAG GAT GTC ACC CCA GAC GCA TGG CCA ACC TGG CCG GTA AAA CTG GGT TGG  
Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val Lys Leu Gly Trp  
CTG ACA CCG CGN GGT GGT GAG CTA ATC GCC TAT CTC GGA CAT TAC CAA CGC  
Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu Gly His Tyr Gln Arg  
CAG CGT CTG GTA GCC GAC GGA TTG CTG GCG AAA AAG GGC TGC CCG CAG TCT  
Gln Arg Leu Val Ala Asp Gly Leu Leu Ala Lys Lys Gly Cys Pro Gln Ser  
GGT CAG GTC GCG ATT ATT GCT GAT GTC GAC GAG CGT ACC CGT AAA ACA GGC  
Gly Gln Val Ala Ile Ile Ala Asp Val Asp Glu Arg Thr Arg Lys Thr Gly  
GAA GCC TTC GCC GCC GGG CTG GCA CCT GAC TGT GCA ATA ACC GTA CAT ACC  
Glu Ala Phe Ala Ala Gly Leu Ala Pro Asp Cys Ala Ile Thr Val His Thr  
CAG GCA GAT ACG TCC AGT CCC GAT CCG TTA TTT AAT CCT CTA AAA ACT GGC  
Gln Ala Asp Thr Ser Pro Asp Pro Leu Phe Asn Pro Leu Lys Thr Gly  
GTT TGC CAA CTG GAT AAC GCG AAC GTG ACT GAC GCG ATC CTC AGC AGG GCA  
Val Cys Gln Leu Asp Asn Ala Asn Val Thr Asp Ala Ile Leu Ser Arg Ala  
GGA GGG TCA ATT GCT GAC TTT ACC GGG CAT CGG CAA ACG GCG TTT CGC GAA  
Gly Gly Ser Ile Ala Asp Phe Thr Gly His Arg Gln Thr Ala Phe Arg Glu  
CTG GAA CGG GTG CTT AAT TTT CCG CAA TCA AAC TTG TGC CTT AAA CGT GAG  
Leu Glu Arg Val Leu Asn Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu  
AAA CAG GAC GAA AGC TGT TCA TTA ACG CAG GCA TTA CCA TCG GAA CTC AAG  
Lys Gln Asp Glu Ser Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys  
GTG AGC GCC GAC AAT GTC TCA TTA ACC GGT GCG GTA AGC CTC GCA TCA ATG  
Val Ser Ala Asp Asn Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met  
CTG ACG GAG ATA TTT CTC CTG CAA CAA GCA CAG GGA ATG CCG GAG CCG GGG  
Leu Thr Glu Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly  
TGG GGA AGG ATC ACC GAT TCA CAC CAG TGG AAC ACC TTG CTA AGT TTG CAT  
Trp Gly Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His  
AAC GCG CAA TTT TAT TTG CTA CAA CGC ACG CCA GAG GTT GCC CGC AGC CGC  
Asn Ala Gln Phe Tyr Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser Arg  
GCC ACC CCG TTA TTG GAT TTG ATC ATG GCA GCG TTG ACG CCC CAT CCA CCG

FIGURE 1 CONT'D

Ala Thr Pro Leu Leu Asp Leu Ile Met Ala Ala Leu Thr Pro His Pro Pro  
 CAA AAA CAG GCG TAT GGT GTG ACA TTA CCC ACT TCA GTC CTG TTT ATT GCC  
 Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu Phe Ile Ala  
 GGA CAC GAT ACT AAT CTG GCA AAT CTC GGC GGC GCA CTG GAG CTC AAC TGG  
 Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu Glu Leu Asn Trp  
 ACG CTT CCC GGT CAG CCG GAT AAC ACG CCG CCA GGT GGT GAA CTG GTG TTT  
 Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly Gly Glu Leu Val Phe  
 GAA CGC TGG CGT CGG CTA AGC GAT AAC AGC CAG TGG ATT CAG GTT TCG CTG  
 Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln Trp Ile Gln Val Ser Leu  
 GTC TTC CAG ACT TTA CAG CAG ATG CGT GAT AAA ACG CCG CTG TCA TTA AAT  
 Val Phe Gln Thr Leu Gln Gln Met Arg Asp Lys Thr Pro Leu Ser Leu Asn  
 ACG CCG CCC GGA GAG GTG AAA CTG ACC CTG GCA GGA TGT GAA GAG CGA AAT  
 Thr Pro Pro Gly Glu Val Lys Leu Thr Leu Ala Gly Cys Glu Glu Arg Asn  
 GCG CAG GGC ATG TGT TCG TTG GCA GGT TTT ACG CAA ATC GTG AAT GAA GCA  
 Ala Gln Gly Met Cys Ser Leu Ala Gly Phe Thr Gln Ile Val Asn Glu Ala  
 CGC ATA CCG GCG TGC AGT TTG AGA TCT CAT CAC CAT CAC TAA 1323  
 Arg Ile Pro Ala Cys Ser Leu Arg Ser His His His His His His His End

**FIGURE 2**  
**pH/Temperature Profile and Stability**



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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: KRETZ
- (ii) TITLE OF INVENTION: NOVEL PHYTASE
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Fish & Richardson P.C.
  - (B) STREET: 4225 Executive Square, Suite 1400
  - (C) CITY: La Jolla
  - (D) STATE: California
  - (E) COUNTRY: US
  - (F) ZIP: 92037
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/910,798
  - (B) FILING DATE: August 13, 1997
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: HAILE, PH.D., LISA A.
  - (B) REGISTRATION NUMBER: 38,347
  - (C) REFERENCE/DOCKET NUMBER: 09010/029001
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 619/678-5070
  - (B) TELEFAX: 619/678-5099

-2-

## (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1272 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: PHYTASE

(ix) FEATURE:  
 (A) NAME/KEY:  
 (B) LOCATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG AAA GCG ATC TTA ATC CCA TTT TTA TCT CTT CTG ATT CCG TTA ACC	48
Met Lys Ala Ile Leu Ile Pro Phe Leu Ser Leu Leu Ile Pro Leu Thr	
1 5 10 15	
CCG CAA TCT GCA TTC GCT CAG AGT GAG CCG GAG CTG AAG CTG GAA AGT	96
Pro Gln Ser Ala Phe Ala Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser	
20 25 30	
GTG GTG ATT GTC AGT CGT CAT GGT GTG CGT GCT CCA ACC AAG GCC ACG	144
Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr	
35 40 45	
CAA CTG ATG CAG GAT GTC ACC CCA GAC GCA TGG CCA ACC TGG CCG GTA	192
Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val	
50 55 60	
AAA CTG GGT TGG CTG ACA CCG CGN GGT GGT GAG CTA ATC GCC TAT CTC	240
Lys Leu Gly Trp Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu	
65 70 75 80	
GGA CAT TAC CAA CGC CAG CGT CTG GTA GCC GAC GGA TTG CTG GCG AAA	288
Gly His Tyr Gln Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Ala Lys	
85 90 95	
AAG GGC TGC CCG CAG TCT GGT CAG GTC GCG ATT ATT GCT GAT GTC GAC	336
Lys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp	
100 105 110	
GAG CGT ACC CGT AAA ACA GGC CAG GCA GAT ACG TCC AGT CCC GAT CCG	384
Glu Arg Thr Arg Lys Thr Gly Gln Ala Asp Thr Ser Ser Pro Asp Pro	
115 120 125	
TTA TTT AAT CCT CTA AAA ACT GGC GTT TGC CAA CTG GAT AAC GCG AAC	432
Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala Asn	
130 135 140	
GTG ACT GAC GCG ATC CTC AGC AGG GCA GGA GGG TCA ATT GCT GAC TTT	480
Val Thr Asp Ala Ile Leu Ser Arg Ala Gly Gly Ser Ile Ala Asp Phe	
145 150 155 160	
ACC GGG CAT CGG CAA ACG GCG TTT CGC GAA CTG GAA CGG GTG CTT AAT	528
Thr Gly His Arg Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu Asn	
165 170 175	

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TTT CCG CAA TCA AAC TTG TGC CTT AAA CGT GAG AAA CAG GAC GAA AGC Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu Ser 180 185 190	576
TGT TCA TTA ACG CAG GCA TTA CCA TCG GAA CTC AAG GTG AGC GCC GAC Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala Asp 195 200 205	624
AAT GTC TCA TTA ACC GGT GCG GTA AGC CTC GCA TCA ATG CTG ACG GAG Asn Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr Glu 210 215 220	672
ATA TTT CTC CTG CAA CAA GCA CAG GGA ATG CCG GAG CCG GGG TGG GGA Ile Phe Leu Leu Gln Ala Gln Gly Met Pro Glu Pro Gly Trp Gly 225 230 235 240	720
AGG ATC ACC GAT TCA CAC CAG TGG AAC ACC TTG CTA AGT TTG CAT AAC Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His Asn 245 250 255	768
GCG CAA TTT TAT TTG CTA CAA CGC ACG CCA GAG GTT GCC CGC AGC CGC Ala Gln Phe Tyr Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser Arg 260 265 270	816
GCC ACC CCG TTA TTG GAT TTG ATC ATG GCA GCG TTG ACG CCC CAT CCA Ala Thr Pro Leu Leu Asp Leu Ile Met Ala Ala Leu Thr Pro His Pro 275 280 285	864
CCG CAA AAA CAG GCG TAT GGT GTG ACA TTA CCC ACT TCA GTA CTG TTT Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu Phe 290 295 300	912
ATT GCC GGA CAC GAT ACT AAT CTG GCA AAT CTC GGC GGC GCA CTG GAG Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu Glu 305 310 315 320	960
CTC AAC TGG ACG CTT CCC GGT CAG CCG GAT AAC ACG CCG CCA GGT GGT Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly Gly 325 330 335	1008
GAA CTG GTG TTT GAA CGC TGG CGT CGG CTA AGC GAT AAC AGC CAG TGG Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln Trp 340 345 350	1056
ATT CAG GTT TCG CTG GTC TTC CAG ACT TTA CAG CAG ATG CGT GAT AAA Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp Lys 355 360 365	1104
ACG CCG CTG TCA TTA AAT ACG CCG CCC GGA GAG GTG AAA CTG ACC CTG Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr Leu 370 375 380	1152
GCA GGA TGT GAA GAG CGA AAT GCG CAG GGC ATG TGT TCG TTG GCA GGT Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala Gly 385 390 395 400	1200
TTT ACG CAA ATC GTG AAT GAA GCA CGC ATA CCG GCG TGC AGT TTG AGA Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu Arg 405 410 415	1248
TCT CAT CAC CAT CAC CAT CAC TAA Ser His His His His His 420	1272

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## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Lys Ala Ile Leu Ile Pro Phe Leu Ser Leu Leu Ile Pro Leu Thr  
 1 5 10 15  
 Pro Gln Ser Ala Phe Ala Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser  
 20 25 30  
 Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr  
 35 40 45  
 Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val  
 50 55 60  
 Lys Leu Gly Trp Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu  
 65 70 75 80  
 Gly His Tyr Gln Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Ala Lys  
 85 90 95  
 Lys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp  
 100 105 110  
 Glu Arg Thr Arg Lys Thr Gly Gln Ala Asp Thr Ser Ser Pro Asp Pro  
 115 120 125  
 Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala Asn  
 130 135 140  
 Val Thr Asp Ala Ile Leu Ser Arg Ala Gly Gly Ser Ile Ala Asp Phe  
 145 150 155 160  
 Thr Gly His Arg Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu Asn  
 165 170 175  
 Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu Ser  
 180 185 190  
 Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala Asp  
 195 200 205  
 Asn Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr Glu  
 210 215 220  
 Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly Trp Gly  
 225 230 235 240  
 Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His Asn  
 245 250 255  
 Ala Gln Phe Tyr Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser Arg  
 260 265 270  
 Ala Thr Pro Leu Leu Asp Leu Ile Met Ala Ala Leu Thr Pro His Pro  
 275 280 285  
 Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu Phe  
 290 295 300  
  
 Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu Glu  
 305 310 315 320  
 Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly Gly  
 325 330 335  
 Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln Trp  
 340 345 350  
 Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp Lys  
 355 360 365  
 Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr Leu  
 370 375 380  
 Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala Gly  
 385 390 395 400  
 Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu Arg  
 405 410 415  
 Ser His His His His His

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420

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:  
(A) NAME/KEY:  
(B) LOCATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GTTTCTGAAT TCAAGGAGGA ATTTAAATGA AAGCGATCTT AATCCCATT

49

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:  
(A) NAME/KEY:  
(B) LOCATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GTTTCTGGAT CCTTACAAAC TGCACGCCGG TAT

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## INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US98/16728

## A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) :Please See Extra Sheet.

US CL :Please See Extra Sheet.

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 426/53, 656; 435/6, 196, 325, 320.1, 252.3; 530/387.9, 388.26; 536/23.1, 23.2, 24.3

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

Please See Extra Sheet.

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category <sup>a</sup>	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	DASSA, J. et al. The Complete Nucleotide Sequence of the Escherichia coli Gene appA Reveals Significant Homology between pH 2.5 Acid Phosphatase and Glucose-1-Phosphatase. J. Bacteriol. September 1990, Vol. 172, No. 9, pages 5497-5500, especially page 5498.	18 ----- 10-12, 31
X	US 5,436,156 A (VAN GORCOM et al.) 25 July 1995, col. 5, lines 10-34.	16
X	Database GenBank on STN. DOEBELI, H. et al. 'Oligonucleotide sequence (adaptor 9) from patent EP0282042'. GenBank. January 1994. Accession No. A02249.	19-23, 25 ----- 26,27

 Further documents are listed in the continuation of Box C.  See patent family annex.

•	Special categories of cited documents:	"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"A"	document defining the general state of the art which is not considered to be of particular relevance	"X"	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"B"	earlier document published on or after the international filing date	"Y"	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"C"	document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"A"	document member of the same patent family
"D"	document referring to an oral disclosure, use, exhibition or other means		
"E"	document published prior to the international filing date but later than the priority date claimed		

Date of the actual completion of the international search

13 OCTOBER 1998

Date of mailing of the international search report

23 OCT 1998

Name and mailing address of the ISA/US  
Commissioner of Patents and Trademarks  
Box PCT  
Washington, D.C. 20231  
Facsimile No. (703) 305-3230

Authorized officer

PETER TUNG

Telephone No. (703) 308-0196



**INTERNATIONAL SEARCH REPORT**

International application No.  
PCT/US98/16728

**A. CLASSIFICATION OF SUBJECT MATTER:**

IPC (6): A23B 7/10; A23J 1/00; C07K 16/12; C07H 15/11, 21/02, 21/04; C12N 9/16, 15/85, 15/63, 1/20; C12Q 1/68

**A. CLASSIFICATION OF SUBJECT MATTER:**

US CL : 426/53, 656; 435/6, 196, 325, 320.1, 252.3; 530/387.9, 388.26; 536/23.1, 23.2, 24.3

**B. FIELDS SEARCHED**

Electronic data bases consulted (Name of data base and where practicable terms used):

MacPar Search (DNA and Protein sequences), APS, MEDLINE, CAPLUS, CANCERLIT, BIOSIS, EMBASE, WPIDS,  
DISSABS

search terms: Keith Kretz, phytase, antibody, feed, E. coli, bacteria

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